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OM protein - protein search, using sw model

Run on: February 11, 2002, 13:31:13 ; Search time 27.64 Seconds
(without alignments)
1725.209 Million cell updates/sec

Title: US-09-553-431-2
Perfect score: 1654
Sequence: 1 MASLRFTNHOSLLPSSL.....KAVVEEPKRGFFSPFCG 326

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

* Database :
1: SPREMBL_17:*
2: SP_Archaea:*
3: SP_Bacteria:*
4: SP_Fungi:*
5: SP_Human:*
6: SP_Invertebrate:*
7: SP_Mammal:*
8: SP_Mhc:*
9: SP_Organelle:*
10: SP_Phage:*
11: SP_Plant:*
12: SP_Rodent:*
13: SP_Virus:*
14: SP_Vertebrate:*
15: SP_Unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1654	100.0	326	10 Q9MBA2	Q9MBA2 Arabidopsis
2	1175.5	71.1	295	10 Q9FV40	Q9FV40 Tagetes
3	1067.5	64.5	306	10 Q9LWY6	Q9LWY6 Oryza sativa
4	756	45.7	274	8 Q9R3P6	Q9R3P6 Nepenthes
5	752	45.5	359	8 Q9R3P6	Q9R3P6 Nepenthes
6	573.5	34.7	276	8 Q9RMB7	Q9RMB7 Proteobacteria
7	536.5	32.4	264	2 Q9K8H9	Q9K8H9 Bacillus
8	516	31.2	262	2 Q67033	Q67033 Aquifex
9	514.5	31.1	269	2 Q9PD08	Q9PD08 Xylella
10	480.5	29.1	271	2 Q9HYZ6	Q9HYZ6 Pseudomonas
11	479	29.0	179	10 Q9SPPO	Q9SPPO Oryza sativa
12	468	28.3	276	2 Q9KQNB	Q9KQNB Vibrio chol
13	449.5	27.2	271	2 Q9JQY6	Q9JQY6 Neisseria
14	449.5	27.2	271	2 Q9AG19	Q9AG19 Neisseria
15	366	22.1	260	1 Q9V165	Q9V165 Pyrococcus
16	344.5	20.8	259	1 Q27868	Q27868 Methanobact
17	341.5	20.3	245	1 Q58346	Q58346 Pyrococcus
18	335	20.3	263	1 Q29562	Q29562 Archaeoglob
19	327.5	19.8	245	1 Q9UY50	Q9UY50 Pyrococcus

20	266	16.1	252	1 Q59470	Q59470 Pyrococcus
21	262.5	15.9	305	1 Q9HNP1	Q9HNP1 Halobacteri
22	254	15.4	217	1 Q59249	Q59249 Pyrococcus
23	250	15.1	319	2 Q9L775	Q9L775 Xanthomonas
24	249	15.1	280	2 Q9RGE0	Q9RGE0 Pseudomonas
25	247.5	15.0	251	1 Q9VIR2	Q9VIR2 Pyrococcus
26	246.5	14.9	288	2 Q9KAS4	Q9KAS4 Bacillus
27	243.5	14.7	323	1 Q9HOY5	Q9HOY5 Halobacteri
28	241	14.6	268	2 Q9P756	Q9P756 Campylobact
29	239.5	14.5	304	2 Q56340	Q56340 Treponema
30	238.5	14.4	305	2 Q44911	Q44911 Borrelia
31	238	14.4	112	2 Q9AENS	Q9AENS Burkholderi
32	236.5	14.3	281	2 Q44757	Q44757 Borrelia
33	236	14.3	275	2 Q87380	Q87380 Pseudomonas
34	230	13.9	294	2 Q25678	Q25678 Helicobacte
35	228	13.8	313	2 Q9K0D3	Q9K0D3 Vibrio chol
36	227	13.7	295	2 Q9L816	Q9L816 Vibrio para
37	224	13.5	294	2 Q9ZM33	Q9ZM33 Helicobacte
38	218	13.2	273	2 Q9Z557	Q9Z557 Zymomonas
39	209.5	12.7	378	2 Q83825	Q83825 Treponema
40	204.5	12.4	278	2 Q67267	Q67267 Aquilex
41	202	12.2	297	1 Q9VOC7	Q9VOC7 Pyrococcus
42	197	11.9	300	1 Q58711	Q58711 Pyrococcus
43	196.5	11.9	295	1 Q9VOD9	Q9VOD9 Pyrococcus
44	196	11.9	382	2 Q9K768	Q9K768 Vibrio chol
45	195	11.8	288	2 Q9X117	Q9X117 Thermotoga

ALIGNMENTS

RESULT	ID	Q9MBA2	PRELIMINARY:	PRT:	326 AA.
Q9MBA2	Q9MBA2	Q9MBA2			
AC	Q9MBA2	Q9MBA2			
DT	01-OCT-2000	(TREMURel. 15, Created)			
DT	01-OCT-2000	(TREMURel. 15, Last sequence update)			
DT	01-JUN-2001	(TREMURel. 17, Last annotation update)			
DE	MIND	(SEPTUM SITE-DETERMINING MIND).			
GN	MIND.				
OS	Arabidopsis thaliana (Mouse-ear cross).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.				
OX	NCBI_TaxID-3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Kum M., Fujiwara M., Kanamaru K., Tanaka K., Takahashi H.;				
RT	"Arabidopsis thaliana mind homolog involved in plastid division."				
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.				
RC	[2]				
RP	SEQUENCE FROM N.A.				
RA	STRAIN-COLUMBIA:				
RX	MEDLINE-98290546; PubMed-9628582;				
RA	Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,				
RA	Tabata S.;				
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. IV.				
RT	physically assigned PI and TAC clones."				
RL	DNA Res. 5:41-54 (1998).				
DR	EMBL: AB030278; BAA90261.1; -				
DR	EMBL: AB009056; BAB08725.1; -				
DR	InterPro: IPR000707; Para.				
DR	Pfam: PRC0991; Para. 1				
SQ	SEQUENCE 326 AA; 35690 MW; BE7AEF4307167825 CXC64;				

Query Match

Best Local Similarity 100.0%; Score 1654; DB 10; Length 326;
Matches 326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLRFTNHOSLLPSSL.....KAVVEEPKRGFFSPFCG 326
|||||

Db	1	MASLLEFSTNHOSILLPSSLSQKLTIISSPRVNNPSRRSPIRSVLOJNRNRPDELAGEPRI	60
Oy	61	VWTSKSGKGVKRTTNTAVGSLIAPYGSVYADADGICIRLDDLLEBRVNTCEVI	120
Db	61	VWTSKSGKGVGTTTITAVGSLIARKYGSVYADADGILRNLDDLLEBRVNTCEVI	120
Oy	121	NGDCRLDQALVRDKRWSNFELLCISKPSKILPMFGGKALEMVLDAKTRPEGSPDII	180
Db	121	NGDCRLDQALVRDKRWSNFELLCISKPSKILPMFGGKALEMVLDAKTRPEGSPDIII	180
Oy	181	DCPAGIDAGFTIATTPANEAVLVITPTTALRDADRYTGLECGIDIKIMYRVTDM	240
Db	181	DCPACIDAGFTIATTPANEAVLVITPTTALRDADRYTGLECCGIDIKIMYRVTDM	240
Oy	241	IKGEDMMSVLVQEMLTSLGLVITPEDESEVIRSTNRKFPVLVINKPPTLAGIAEQAAARL	300
Db	241	IKGEDMMSVLVQEMLTSLGLVITPEDESEVIRSTNRGFPVLVINKPPTLAGIAEQAAARL	300
Oy	301	VEQDSMKAVMYEEPPKKRGFFSFFGG	326
Db	301	VEQDSMKAVMYEEPPKKRGFFSFFGG	326

RESULT	2		
09FV40			
ID	09FV40	PRELIMINARY:	PRT: 295 AA.
AC	09FV40.		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	MIND.		
OS	Tagetes erecta (African marigold).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
CC	Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;		
CC	Heliantheae; Tagetes.		
OX	NCBI_TaxID=13708;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Moehs C.P., Tian L., DellaPenna D.;		
RT	"Analysis of carotenoid biosynthetic gene expression during marigold		
RT	petal development.";		
RL	Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AF251019; AAG10431.1; -.		
DR	InterPro: IPR000707; Para.		
DR	Pfam: PF00991; Para. 1		
SO	SEQUENCE 295 AA; 32756 MW; 212BD4765F58747F CRC64;		

[illegible]

QY 284 KPPTLAGLAFEQAAWRLVEQDSMKAVMVEEPPKKRGFSFFGG 326
 |||||
 Db 253 KPPTLAGLAFEQAAWRLVEQDSMKAVMVEEPPKKRGFSFFGG 295

RESULT	3	
09LWY6		
ID	09LWY6	PRELIMINARY;
AC	09LWY6	PRF; 306 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	SIMILAR TO CHLORELLA VULGARIS C-27 CHLOROPLAST DNA.	
OS	Oryza sativa (Rice)	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta	
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
OC	Emnataceae; Oryzaeae; Oryza.	
OX	NCBI_TaxID=4530;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CV. NIPPONBARE;	
RA	Sasaki T., Matsumoto T., Yamamoto K.;	
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC	
RT	clone:P0644B06."	
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AP001129; BAA90628.1;	
DR	InterPro; IPR000707; PARA.	
DR	Pfam; PF00991; PARA.1	
SO	SEQUENCE 306 AA; 32341 MW; CECAB38219512650 CRC64;	

	Query Match	64.5%;	Score 1067.5;	DB 10;	Length 306;
	Best Local Similarity	68.4%;	Pred. No. 1.1e-73;		
	Matches 216;	Conservative	31;	Mismatches 50;	Indels 19;
					Gaps 5
QY	14	LLPSSLSQKTLISSPFVNNPSRRSPTRSVLQENRKPELAGETPRIVYITSGKGVGKT	73		
Db	7	LLPSS-----RCPPASSPARRG-----RTAPELISGPRVVYVITSGKGVGKT	51		
QY	74	TTTANVGLSTARQSGVAIDADLDGLRMILLGLGENVNTQCVINGDCGLDALVRD	133		
Db	52	TTTANLALSLARLSANAAVDADAGLRMDLLGLGENVHLTAADVLGDCGLDALVRH	111		
QY	134	KRMSNFELLSCKPSKSLKPMGEGGKALEMLVDALKTREGSPDFTIIDCPADIDAGTTA	193		
Db	112	RALDLDTLLCTSKPSKSLPLAFSGSTLTWVADALR-RAANPAFTLIDCPADVADGFVTA	170		
QY	194	ITPANEAIVLTTPITLALRDADRYTGILCEGIRIKIMIVNRVPTMDIKGEPMSSVLVQ	253		
Db	171	IAPBEAVLVTPDITLALRDADRYAGLECGIKIKITIVNRVPTDVLKGEPMSSALDQ	230		
QY	254	EMGLSLGLVIPEDSEVIRSTNRGFLVLRNKPPTLAGLAFQAAWLVEODSMKAVMEE	313		
Db	231	EMGLPLTLGVPEDEAEVIRSTNRGFLVLRNKPPTLAGLAFQATWRLVERDAMTAVMEE	290		
QY	314	E-PKKR-GPFSFEGG 326			
Db	291	QERPKKRAGPFSFEGG 306			
RESULT	4				
Q9T3P6	Q9T3P6	PRELIMINARY;	PRT;	274 AA.	
AC	Q9T3P6;				
DT	01-MAY-2000 (TEMBLrel. 13, Created)				
DT	01-MAY-2000 (TEMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TEMBLrel. 17, Last annotation update)				
DE	SEPTUM-SITE DETERMINING PROTEIN.				
GN	MIND.				
OS	Nephroselmis olivacea.				
OC	Chloroplast.				
OC	Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;				
CC	Chlorodendraceae; Chlorodendraceae; Nephroselmis.				

OX NCBI_TaxID=31312;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9938694; PubMed=10468594;
 RA Turnell M., Ollis C., Lemieux C.;
 RT "The complete chloroplast DNA sequence of the green alga *Nephroselmis*
 RT *olivaeca*: insights into the architecture of ancestral chloroplast
 RT genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Turnell M., Ollis C., Lemieux C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF137379; AAD54908.1;
 DR EMBL: AF137379; AAD54881.1;
 DR InterPro: IPR000707; Para.
 DR Pfam: PF00991; Para: 1.
 DR Chloroplast.
 SO SEQUENCE 274 AA; 30126 MW; 9D0A1449E6815845 CRC64;

Query Match

Best Local Similarity 45.7%; Score 756; DB 8; Length 274;
 Matches 155; Conservative 39; Mismatches 60; Indels 10; Gaps 3;

OY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRLNLLGLRNVTGVE 118
 DB 14 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRLNLLGLRNVTGVE 118
 DB 119 VINGDRLDQALVDRKMSNFELLCISPRSKLPMFGGKALEMVDALKTREPSDFE 178
 DB 74 VIEGOCRLQALIRDRKMSNFELLCISPRSKLPMFGGKALEMVDALKTREPSDFE 178
 OY 179 IIDCAGTADGTTATTPANEAVLVTPTALRDADVTGCGDGRDKIMVNVRT 238
 DB 129 IIDCAGTADGTTATTPANEAVLVTPTALRDADVTGCGDGRDKIMVNVRT 238
 DB 239 DMKGEDMMSVLDVQEMLSLGLVPESEVIRSTNRGPFVLPKPTAGLAFQAAW 298
 DB 189 EMIQNDMMSVLDVQEMLSLGLVPESEVIRSTNRGPFVLPKPTAGLAFQAAW 298
 OY 299 RIVEDSKAKVAVVEEPRKRGFS 322
 DB 249 RLVGLPS-----PSDSAPSRGWFA 267

RESULT 5
 OY 09JUR6 PRELIMINARY; PRT: 359 AA.
 AC 09JUR6;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CELL DIVISION INHIBITOR MIND.
 GN MIND.
 OS Prototheca wickerhamii.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
 OC Chlorellaceae; Prototheca.
 OX NCBI_TaxID=3111;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Knauf U., Hachtel W.;
 RT "A 22 kb fragment of the 53 kb plastid genome of the colourless alga
 RT *Prototheca wickerhamii* containing atp-, rpl-, rps-, rrr-, and trn-
 RT genes.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ245645; CAB53105.1;
 DR InterPro: IPR000707; Para.
 DR Pfam: PF00991; Para: 1.
 DR Cell division; Chloroplast.
 SO SEQUENCE 359 AA; 40804 MW; E550EAF50BC0A51E CRC64;

Query Match
 Best Local Similarity 45.8%; Score 752; DB 8; Length 359;
 Matches 159; Conservative 44; Mismatches 62; Indels 22; Gaps 5;

OY 35 PSRRSPRSYL-QFNRP-----ELAGE-----PRIVVITSGKGVGKTTT 77
 DB 53 PEERKITEQLQKPSSESEVNTLELDKGDSELEPRVITSGKGVGKTTT 112
 OY 78 NGLSLARYGSVAIDADGLRLNLLGLRNVTGVEVINGDRLDQALVDRKMS 137
 DB 113 NGLSLARYGSVAIDADGLRLNLLGLRNVTGVEVINGDRLDQALVDRKMS 172
 OY 138 NEELCISPRSKLPMFGGKALEMVDALKTREPSDFEIIDCPAGIDGTTATPA 197
 DB 173 NLALLAVSKHOK--VYVQGMHRLVFSIK---ELGINSILDCPAGIDGTTATPA 227
 OY 198 NEAVLVTPTDITRALRDADVTGCGDGRDKIMVNVRTDMKGEDMMSVLDVQEM 257
 DB 228 NEAVLVTPTDITRALRDADVTGCGDGRDKIMVNVRTDMKGEDMMSVLDVQEM 287
 OY 258 LSLGLVPESEVIRSTNRGPFVLPKPTAGLAFQAAWRLVED 304
 DB 288 IFLGALPEDTNTVISTNKGPELVLDKLTLSIAFENMARRLIGKE 334

RESULT 6

OY 09RWB7 PRELIMINARY; PRT: 276 AA.
 AC 09RWB7;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE SEPTUM SITE-DETERMINING PROTEIN.
 GN DR0752.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus; Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RL;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eison J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA McFait K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Uffordback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium *Deinococcus*
 RT *radiodurans* RL.";
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001931; AAF10331.1;
 DR TIGR: DR0752;
 DR InterPro: IPR000392; NitrogenaseII.
 DR InterPro: IPR000707; Para.
 DR Pfam: PF00142; fer4_NifH; 1.
 DR Pfam: PF00991; Para: 1.
 SO SEQUENCE 276 AA; 29420 MW; AD74FDF45820DC CRC64;

Query Match
 Best Local Similarity 44.3%; Score 573.5; DB 2; Length 276;
 Matches 125; Conservative 52; Mismatches 72; Indels 33; Gaps 5;

OY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRLNLLGLRNVTGVE 118
 DB 12 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRLNLLGLRNVTGVE 118
 OY 119 VINGDRLDQALVDRKMSNFELLCISPRSKLPMFGGKALEMVDALKTREPSDFE 178

QY	DB	171	--PEGSPDFIIIDCPAGIDAGFTAITTPANEAIVVTPDITALDADRVYGLLEDCIRD	228
QY	Db	118	LLEEFGFRLVLDSPGAGIESGFTAAAPAEALAVVNEEVSVDADRIIGLLEAQDITE	177
QY	229	IKMIYRVRTMIMGEDMWSVLDVQEMGLSLGVIPEDSVIRSTNNGEFLYENKPPTL	288	
Db	178	IRLVNRRLRPRKMAVSGNNLSIDMDWDILGVAPRFGPEDEBIYSTINGGEAVLGR--TK	235	
QY	289	AGLAFEOAMRLVLEDQSMKAVVVEEPPKRGFFS---FFCG	326	
Db	236	AGDAFMATAORILOGDVPEPKLTEEE--KGIMAIRLRFGG	274	
RESULT	7			
Q9K8H9		PRELIMINARY;	PRT;	264 AA.
AC	Q9K8H9;			
DT	01-OCT-2000 (TREMBLrel. 15, created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)			
DE	SEPTUM SITE-DETERMINING PROTEIN.			
GN	MIND OR BH3027.			
OS	Bacillus halodurans.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
OX	Bacillus/Staphylococcus group; Bacillus.			
NCBI_Taxid=86665;				
RP	SEQUENCE FROM N.A.			
RC	STRAIN-C-125 / JCM 9153;			
RX	MEDLINE=20512582; PubMed=11058132.			
RA	Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,			
RA	Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,			
RA	Horikoshi K.;			
RT	"Complete genome sequence of the alkaliphilic bacterium Bacillus			
RT	halodurans and genomic sequence comparison with Bacillus subtilis.";			
RL	Nucleic Acids Res. 28:4317-4331(2000).			
DR	EMBL; AF001517; BAB06746.1; -			
DR	InterPro; IPR000392; NtRCGaseSet1.			
DR	InterPro; IPR000707; PARA.			
DR	Pfam; PF00142; fer4_N1FH.1.			
DR	Pfam; PF00991; Para; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 264 AA; 28818 MW; 78D523BEB583172F CRC64;			
Query Match	32.4%;	Score 536.5;	DB 2;	Length 264;
Best Local Similarity	41.1%;	Pred. No. 2.9e-33;		
Matches 109;	Conservative 66;	Mismatches 83;	Indels 7;	Gaps 3;
QY	61	VVTSKSGGKTKTTTANVGLSLARGFSSVAITDALGLRNDLLGLENRVNVCVEVI	120	
Db	5	IVTSGGGKTKTTSTNIGTALALSGKVCVLDVTDIGLRNDVYVNGLEIRIITDLDVYV	64	
QY	121	NGDCRLDQALVVRDKRMSNFELCTISKPRSKLPMFGCGKALEWLVDALKTRPEGSPDFII	180	
Db	65	EGRGRLKQALIKKRFECULNLPAAQTKDK--SAYVPEQKKEIVEELKQ---EYDYVLI	118	
QY	181	DCPAGIDAGFTAITTPANEAIVVTPDITALDADRVYGLLEDCGIRDIKMIYRVRTM	240	
Db	119	DCPAGIEGFRKNVAVGADKAIVVTPPEISVRADRIIGLLEKEVEAPRLVNRIGHM	178	
QY	241	IKGDDMSVLDVQEMGLSLGVIPEDSVIRSTNNGEFLYENKPPTLGLAFEOAMRL	300	
Db	179	MKNGEMDVEIYSITALELGLIVDDEENVIKSNKEPILAH-PSDKASVAIRNLARI	237	
QY	301	VEQDSMKAVVVEEPPKRGFFSFFG	325	
Db	238	LGFTVPLMSFQEKGVLAIKISFFG	262	
RESULT	8			

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ID 067033 PRELIMINARY; PRT; 262 AA.
AC 067033:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SEPTUM SITE-DETERMINING PROTEIN MIND.
GN MIND2 OR AQ_877.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPS;
RX MEDLINE=98196666; PubMed=9537320;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snad M.A., Keller M., Anujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.D., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
RD EMBL: AE000712; AAC06996.1;
RD InterPro: IPR000392; NitrogenaseII.
DR InterPro: IPR000707; PARA.
DR Pfam: PF00142; fer4_NiFe; 1.
DR Pfam: PF00991; Para; 1.
KW Complete proteome.
SQ SEQUENCE 262 AA; 28913 MW; 535C2E5F3D5B352A CRC64;

Query Match 31.2%; Score 516; DB 2; Length 262;
Best Local Similarity 41.4%; Pred. No. 1.le-31;
Matches 108; Conservative 65; Mismatches 70; Indels 18; Gaps

QY 60 IVVITSGKGGVKTITTTANVGISLARVPSSVAIDADIGLBNLDLLGLEKRVYITVEV 119
   :::::::::::::: ::::: : : ::::: ::::: ::::: ::::: : : ::
DB 4 VIIVTSGKGGVKTITTTANIGTALAKTKKVVLLIDADIGLBNLDLLGLEKRVYIDLV 63
   :::::::::::::: ::::: : : ::::: ::::: ::::: ::::: : : ::
QY 120 INDCDGLDALVRDKRWSNFELTISKPSRKLPMGFGSKALEMFLVDALKTRESSPDFII 179
   :::::::::::::: ::::: : : ::::: ::::: ::::: ::::: : : ::
DB 64 LBSRVEYEAALVKDKRGLSLMLLPANQANKDIVDIE-----KMKKTYEELKNSGNYDYL 119
   :::::::::::::: ::::: : : ::::: ::::: ::::: ::::: : : ::
QY 180 IDCPCADIGFTTITPANEAVALVTPDITLALRDADRYTGLLCEDGIDIMIVNRRPTD 235
   :::::::::::::: ::::: : : ::::: ::::: ::::: ::::: : : ::
DB 120 VDSPCIIEKGFOIAVSPADKALIVNPEVSSIRDDADRYIGLLESMKDKNRYIVNRKWE 179
   :::::::::::::: ::::: : : ::::: ::::: ::::: ::::: : : ::
QY 240 MKEGEMMSVLDVQEWLGLSLIGVIPESDEVSRSNRGPPVLYLNK--PPTLAGIAFEQAA 297
   :::::::::::::: ::::: : : ::::: ::::: ::::: ::::: : : ::
DB 180 MVRGAMLSVEDVLDLKEITIGIIPEEKVLDFYNRGEPYLVLEKFPASQAII----- 235
   :::::::::::::: ::::: : : ::::: ::::: ::::: ::::: : : ::
QY 298 WRLVEDDSMKAAVVEDEPKR 318
   :::::::::::::: ::::: : : ::::: ::::: ::::: ::::: : : ::
DB 234 -----DFARLMGESIPLEKR 248
   :::::::::::::: ::::: : : ::::: ::::: ::::: ::::: : : ::

RESULT 9
Q9PD08 PRELIMINARY; PRT; 269 AA.
AC Q9PD08:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SEPTUM SITE-DETERMINING PROTEIN.
GN xrl321.
OS xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC SMRAN=945C;
RX MEDLINE=20365717; PubMed=10910347;
RA Stimpson A.J.G., Reznach F.C., Arruda P., Abreu F.A., Acencio M.,

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RA Alverenga R., Alves L.M.C., Araya J.F., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Fachelino A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garlier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.T.,
 RA Menck C.F.M., Miraca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhami A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Trufil D., Tsai S.M., Tsubako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Zeldanis J., Zetubal J.C.,
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*,"
 RT Nature 406:151-159(2000).
 DR EMBL: AE003965; AAF84130.1;
 DR InterPro: IPR000392; NitrogenaseII.
 DR InterPro: IPR000707; Para.
 DR Pfam: PF00142; fer4_N1FH; 1.
 DR Pfam: PF00991; Para; 1.
 DR Complete proteome.
 SQ SEQUENCE 269 AA; 28823 MW; CC9A5DE80BC06A26 CRC64;

Query Match 31.1%; Score 514.5; DB 2; Length 269;
 Best Local Similarity 43.5%; Pred. No. 1.4e-31;
 Matches 120; Conservative 58; Mismatches 79; Indels 19; Gaps 8;

QY 60 IYVITSGKGVGKTTTANGSLARYGFSVAIDADLGRNLDLGLGNRYNTCYEV 119
 DB 4 IYVITSGKGVGKTTTANGSLARYGFSVAIDADLGRNLDLGLGNRYNTCYEV 63
 QY 120 INDCRLDQALVDRKMSNFELLCISPRSKLPMFGCGKALEMVDALKTREPSDPII 179
 DB 64 IDGEATLKALIKDKRFDNYLLAAOTRKDALTRKS--VEKYLNELQA--EGF-DYIC 118
 QY 180 IDCPAGIDAGFTAITPANEAVALVTPDITARDARVYGL-----ECGDIRDIKMT 232
 DB 119 CDSFACIEGASLAMYFADAVVAVVNEVSSVRSDRIIGLDSKTKRAEFGSIITLL 178
 QY 233 VNRVTRDMIKGEDMSVLDVQEMGLSLGVIPEDSEVINSTNGCFPLVLPKPTLACIA 292
 DB 179 LFRYSPARVESGEMSLADVEVLGKALGVIPESGVLNANSNGEPVILDN-NSLAGLA 237
 QY 293 FEGQAMRLVEOD-SMKAVMYEEPRKRGFS-FRFG 326
 DB 238 YEDAVGRILGEDHPMRTVE---KKGFSKLEFG 269

RESULT 10
 Q9HYZ6 PRELIMINARY: PRT; 271 AA.
 AC Q9HYZ6: 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DR CELL DIVISION INHIBITOR MIND.
 OS MIND OR PA3244.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.

OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Gardner R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lapidis K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 RT opportunistic pathogen,"
 RT Nature 406:959-964(2000).
 DR EMBL: AE004747; AAC06632.1;
 DR InterPro: IPR000707; Para.
 DR Pfam: PF00991; Para; 1.
 DR Complete proteome.
 SQ SEQUENCE 271 AA; 29635 MW; 0367E2BC42A06444 CRC64;

Query Match 29.1%; Score 480.5; DB 2; Length 271;
 Best Local Similarity 39.6%; Pred. No. 5.6e-29;
 Matches 113; Conservative 54; Mismatches 83; Indels 35; Gaps 7;

QY 59 RIVVITSGKGVGKTTTANGSLARYGFSVAIDADLGRNLDLGLGNRYNTCYEV 118
 DB 3 RIVVITSGKGVGKTTTANGSLARYGFSVAIDADLGRNLDLGLGNRYNTCYEV 62
 QY 119 VINGCDRLDQALVDRKMSNFELLCISPRSKLPMFGCGKALEMVDALKTREPSDPII 172
 DB 63 VINGCDRLDQALVDRKMSNFELLCISPRSKLPMFGCGKALEMVDALKTREPSDPII 108
 QY 173 GSPDF--ITIDCPAGIDAGFTAITPANEAVALVTPDITARDARVYGLLECDGIRDIK 230
 DB 109 LKDFEYIICDSPAGIEKHAHLAMYFADAVVAVVNEVSSVRSDRIIGLDSKTKRAEFGSIITLL 168
 QY 231 -----MIVNRVTRDMIKGEDMSVLDVQEMGLSLGVIPEDSEVINSTNGCFPLV 282
 DB 169 GEPKIEHLLRTRYNPERYTKGEMIGVDVEELIARLGLVIPSQVAKNAGVYVIL 228
 QY 283 NRPTPLAGLAFEGQAMRLVEODSMKAVMYEEPRKRGFS-FRFG 326
 DB 229 DQSD-AGQAVSDAVDRLLGKEIPHREL---DVOKKGFLGRLEGG 269

RESULT 11
 Q9SPPO PRELIMINARY: PRT; 179 AA.
 AC Q9SPPO: 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DR CELL DIVISION INHIBITOR MIND HOMOLOG (FRAGMENT).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocarpaceae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. IR-BB21;
 RA Han F., Kilian A., Chen J.P., Kudrna D., Steffenson B., Yamamoto K.,
 RA Matsunoto T., Sasaki T., Kleinof A.,
 RT "Sequence analysis of a rice BAC covering the syntenous barley Rpg1
 RT region,"
 RL Genome 0:0-0(1999).
 DR EMBL: AF149810; AAF00142.1;
 DR InterPro: IPR000392; NitrogenaseII.
 DR Pfam: PF00142; fer4_N1FH; 1.
 OR Cell division.
 FT NON-TER 179 179
 SQ SEQUENCE 179 AA; 18705 MW; 3DE6FA7D6E76E77 CRC64;

Query Match 29.0%; Score 479; DB 10: Length 179;
Best Local Similarity 57.1%; Pred. No. 4.1e-29;
Matches 100; Conservative 19; Mismatches 40; Indels 16; Gaps 3;

```
QY 14 LLLPSSLSQKTLISSPFRVNNPSRRSPILSVLOENRKPBLAGEPRIVITSGKGVGKT 73
   |||||
   7 LLLPSS-----RCPPEASSPARHG-----RTAPELSGPRVAVVITSGKGVGKT 51
   |||||

QY 74 TTTANNGSLARIGFVYVALDADGLRNDLLGLERNVNTCEVINGDCRLDQALVRD 133
   |||||
   52 TTTANLAASLARISLSAVADADAGLRNDLLGLERNVNTCEVINGDCRLDQALVRH 111
   |||||

QY 134 KRNSFELLICISPRSKLPMFGGKALEMLVDALKTREGSPDFTIIDCPAGIDA 188
   : : : : : |||||
   DB 112 RALHDQLQLLSKRPSKPLAFSGSKITLWADALR-RAANPAFILIDCPAGQSA 165
   : : : : : |||||

RESULT 12
O9KON8 PRELIMINARY; PRT; 276 AA.
AC O9KON8:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SEPTUM SITE-DETERMINING PROTEIN MIND.
GN VCI1960.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RT Nature 406:477-483(2000).
DR EMBL; AE004271; AAF95108.1; -.
DR TIGR; VCI1960; -.
DR InterPro; IPR000707; Para.
DR Pfam; PF00991; Para; 1.
KW Complete proteome.
SQ SEQUENCE 276 AA; 30098 MW; 46CB44013A847E59 CRC64;
```

Query Match 28.3%; Score 468; DB 2: Length 276;
Best Local Similarity 40.4%; Pred. No. 5.2e-28;
Matches 112; Conservative 57; Mismatches 90; Indels 18; Gaps 7;

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QY 59 RIVVITSGKGVGKTTTANVGLSLARIGFVYVALDADGLRNDLLGLERNVNTCEV 118
   |||||
   DB 9 RIVVITSGKGVGKTTTANVGLSLARIGFVYVALDADGLRNDLLGLERNVNTCEV 68
   |||||

QY 119 VINGDCRLDQALVRDGRKWSNFELLICISPRSKLPMFGGKALEMLVDALKTREGSPDFT 178
   |||||
   DB 69 VINGDCRLDQALVRDGRKWSNFELLICISPRSKLPMFGGKALEMLVDALKTREGSPDFT 123
   |||||

QY 179 IIDCPAGIDAGFTAITPANEAVLVTPDITLADADRVGLLECDGIR-----DIK-- 230
   |||||
   DB 124 ICDSPAGIEGALMALYFADEAVITVTPNEVSVSDRILGILQSKRAEGQAPIKOH 183
   |||||

QY 231 MIVNRVETMIKEDMKSVDLVQEMGLSLGVIPEDSEVIRSTRNRPFLVLPKPTLAG 290
   : : : : : |||||
   DB 184 LILTRVNPARTVGEMLSVDQVEIHLVPLIGVIPSQAVLNASKGVPIVTFDQSD-AG 242
   : : : : : |||||
```

QY 291 LAFEQAMRLV-EQDSKAVAVEEPKRGFFSGG 326
||| : : : |||
DB 243 QAVQDTVARLHSGQVEFRFL---TEAKKGIKFLFGG 276
||| : : : |||

```
RESULT 13
O9JOY6 PRELIMINARY; PRT; 271 AA.
AC O9JOY6:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SEPTUM SITE-DETERMINING PROTEIN (SEPTUM SITE-DETERMINING PROTEIN
DE MIND).
GN MIND OR NMA0100 OR NMB0171.
OS Neisseria meningitidis (serogroup A), and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699; 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Deakin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RT Nature 404:502-506(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouli H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizzoli R., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RT Science 287:1809-1815(2000).
DR EMBL; AL162752; CAB83415.1; -.
DR EMBL; AE002374; AAF40628.1; -.
DR TIGR; NMB0171; -.
DR InterPro; IPR000707; Para.
DR Pfam; PF00991; Para; 1.
KW Complete proteome.
SQ SEQUENCE 271 AA; 29559 MW; 9ACDB52A03BD6170 CRC64;
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Query Match 27.2%; Score 449.5; DB 2: Length 271;
Best Local Similarity 37.5%; Pred. No. 1.3e-26;
Matches 104; Conservative 63; Mismatches 93; Indels 17; Gaps 7;

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QY 59 RIVVITSGKGVGKTTTANVGLSLARIGFVYVALDADGLRNDLLGLERNVNTCEV 118
   |||||
   DB 3 RIVVITSGKGVGKTTTANVGLSLARIGFVYVALDADGLRNDLLGLERNVNTCEV 62
   |||||

QY 119 VINGDCRLDQALVRDGRKWSNFELLICISPRSKLPMFGGKALEMLVDALKTREGSPDFT 178
   |||||
   DB 63 VINGDCRLDQALVRDGRKWSNFELLICISPRSKLPMFGGKALEMLVDALKTREGSPDFT 119
   |||||

QY 179 IIDCPAGIDAGFTAITPANEAVLVTPDITLADADRVGLL-----ECDGIRDIRK 231
   |||||
   DB 120 ICDSPAGIEGALMALYFADEAVITVTPNEVSVSDRILGILQSKRAEGQGSVEHL 179
   |||||

QY 232 IVNRVETMIKEDMKSVDLVQEMGLSLGVIPEDSEVIRSTRNRPFLVLPKPTLAG 291
   : : : : : |||||
```

Db 180 LITRSPERVAKGMLSVQDIDICDILHPLLGVPESQNVLAQNSGEP-VIHODSVAASE 238
 QY 292 AFEQAMRLV-EQDSMKAVVEEPKRGFFS-FFGG 326
 Db 239 AYKDVIALRLGLENREMRFL---EAEKKSFFKRLFGG 271

RESULT 14

Q9AG19 PRELIMINARY: PRT: 271 AA.

AC Q9AG19 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE MIND.
 GN MIND.
 OS *Neisseria gonorrhoeae*.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CH811;
 RC MEDLINE=21097259; PubMed=11160816;
 RA Ramirez-Arcos S., Szeto J., Beveridge T., Victor C., Francis F.,
 RA Dillon J.;
 RT "deletion of the cell-division inhibitor Minc results in lysis of
 RT *Neisseria gonorrhoeae*."
 RL Microbiology 147:225-237 (2001).
 DR EMBL: AF345908; AAK30126.1; -.
 SR SEQUENCE 271 AA; 29597 MW; 87EC6FE31067B542 CRC64;

Query Match 27.2%; Score 449.5; DB 2; Length 271;
 Best Local Similarity 37.5%; Pred. No. 1.3e-26;
 Matches 104; Conservative 63; Mismatches 93; Indels 17; Gaps 7;

QY 59 RIVVITSGKGVGKTTTANNGLSLARYGSVAIDADLGLRNDLLGLNRYNTCVE 118
 Db 3 KIIIVTSGKGVGKTTTANNGLSLARYGSVAIDADLGLRNDLLGLNRYNTCVE 118
 QY 119 VINGDCRLDQALVRDKRNSFELLCISKPRSKLPMGF--GKALEMVDALKTRPES 178
 Db 63 VIQGRATLQALIKKNCENLFLPASQTRDKDALTRG--VEKVMQELSGKKMGF-EYI 119
 QY 179 IIDCPAGIDAGFTTITPANEAVLVTPTDITALRDADRVYGL-----ECGIRDIM 231
 Db 120 ICDSFAGIEOGALMALYFADEAIVTNPVSSVRDSDRILGILQSKSRKAOGGSVKEHL 179
 QY 232 IVNRVRTMIKGEDMMSVLDVQEMGLSLGVIPEDSEVIRSTNRGFPVLNKPPTLAGL 291
 Db 180 LITRSPERVAKGMLSVQDIDICDILHPLLGVPESQNVLAQNSGEP-VIHODSVAASE 238
 QY 292 AFEQAMRLV-EQDSMKAVVEEPKRGFFS-FFGG 326
 Db 239 AYKDVIALRLGLENREMRFL---EAEKKSFFKRLFGG 271

RESULT 15

Q9V165 PRELIMINARY: PRT: 260 AA.

AC Q9V165 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CELL DIVISION INHIBITOR (MIND-1).
 GN PAB1983.
 OS *Pyrococcus abyssi*.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ORSAY;

RA Hellig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 RT structure and evolution";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ248284; CAB49485.1; -.
 DR InterPro: IPR000392; NitrogenaseII.
 DR InterPro: IPR000707; ParaA.
 DR Pfam: PF00142; Ier4_N1FH; 1.
 DR Pfam: PF00991; Para; 1.
 KW Cell division; Complete proteome.
 SR SEQUENCE 260 AA; 27657 MW; 8C02C95C720A35B8 CRC64;

Query Match 22.1%; Score 366; DB 1; Length 260;
 Best Local Similarity 32.9%; Pred. No. 2.9e-20;
 Matches 94; Conservative 54; Mismatches 88; Indels 50; Gaps 7;

QY 59 RIVVITSGKGVGKTTTANNGLSLARYGSVAIDADLGLRNDLLGLNRYNTCVE 118
 Db 4 RSIYFASGKGVGKTTTANNGLSLARYGSVAIDADLGLRNDLLGLNRYNTCVE 118
 QY 119 VINGDCRLDQALVRDKRNSFELLCISKPRSKLPMGF--GKALEMVDALKTRPES 173
 Db 63 VLAEEADLKDVAIEG-----PAGVAVIPGSLERIKKARAEERLDL 104
 QY 174 -----SPDFTIIDCPAGIDAGFTTITPANEAVLVTPTDITALRDADRVYGL 227
 Db 105 IREISQMGDFLIDAPAGLELITALLIGKELIIVTNPETAITDSLTKRVAKELGTL 164
 QY 228 DIKVIIVNRVRTDMIKGEDMMSVLDVQEMGLSLGVIPEDSEVIRSTNRGFPVLNKPPT 287
 Db 165 PLGAILNRVTVSEKTE---LSREIEALELVLTGTPEDPEVKRASAAGVPLVVKNPPTS 220
 QY 288 LAGLAPEQAA-----WRLVEDSMKAVVEEPKRGFFSFFGG 326
 Db 221 PAIAYKEIAKLAGIKKKPPEPS-----PVKRIFRALFGG 257

Search completed: February 11, 2002, 13:32:41
 Job time: 88 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 11, 2002, 13:31:13 ; Search time 24.36 Seconds

(without alignments)
991.293 Million cell updates/sec

Title: US-09-553-431-2

Perfect score: 1654

Sequence: 1 MASLRLFTSTNQSLLPSSL.....KAWVEEPKRGFFSFGG 326

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101:*

- 1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT:*
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- 6: /SIDSR/gcgdata/geneseq/geneseq/AA1985.DAT:*
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- 8: /SIDSR/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDSR/gcgdata/geneseq/geneseq/AA1988.DAT:*
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- 12: /SIDSR/gcgdata/geneseq/geneseq/AA1991.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1654	100.0	326	21	Arabidopsis thaliana
2	1654	100.0	343	21	Arabidopsis thaliana
3	1648	99.6	326	21	Arabidopsis thaliana
4	1648	99.6	344	21	Arabidopsis thaliana
5	888	53.7	174	21	Arabidopsis thaliana
6	888	53.7	174	21	Arabidopsis thaliana
7	224	13.5	294	19	Arabidopsis thaliana
8	224	13.5	297	18	Arabidopsis thaliana
9	209	12.6	425	18	Arabidopsis thaliana
10	206	12.5	388	21	Arabidopsis thaliana
11	198	12.0	412	18	Arabidopsis thaliana

12	197.5	11.9	279	22	AA693171
13	190	11.5	390	22	AA681141
14	183	11.1	313	21	AA611242
15	183	11.1	313	21	AA611242
16	178	10.8	289	22	AA694219
17	176	10.6	288	21	AA690222
18	173.5	10.5	375	22	AA690990
19	171.5	10.4	271	22	AA692570
20	165	10.0	115	21	AA640393
21	164.5	9.9	478	22	AA690129
22	161	9.7	400	21	AA622282
23	161	9.7	400	21	AA622282
24	161	9.7	532	21	AA622282
25	161	9.7	532	21	AA622282
26	161	9.7	547	21	AA639876
27	161	9.7	547	21	AA639876
28	159.5	9.6	257	21	AA622282
29	158.5	9.6	257	21	AA622282
30	154.5	9.3	350	21	AA641434
31	152.5	9.2	296	21	AA641434
32	145	8.8	171	18	AA620504
33	141	8.5	227	21	AA618171
34	128.5	7.8	225	21	AA689905
35	125.5	7.6	231	22	AA689905
36	125	7.6	255	20	AA635442
37	121	7.3	317	20	AA637626
38	120.5	7.3	196	20	AA690007
39	120.5	7.3	242	20	AA690006
40	120.5	7.3	243	20	AA690006
41	118	7.1	261	22	AA691316
42	118	7.1	292	21	AA673353
43	117	7.1	222	21	AA611244
44	117	7.1	222	21	AA643416
45	117	7.1	223	21	AA611243

ALIGNMENTS

RESULT 1	AA646531	standard; protein; 326 AA.
ID	AA646531	
XX	AA646531	
XX	18-OCT-2000 (first entry)	
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 58550.	
DE	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX	Arabidopsis thaliana.	
OS	Arabidopsis thaliana.	
XX	EP103405-A2.	
PN	06-SEP-2000.	
PD	25-FEB-2000; 2000EP-0301439.	
XX	25-FEB-1999; 99US-0121825.	
XX	05-MAR-1999; 99US-0123180.	
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RESULT 2

AAG46530 standard; Protein; 343 AA.

AC AAG46530;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 58549.

KW Protein identification: signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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Query Match 100.0%; Score 1654; DB 21; Length 343;
Best Local Similarity 100.0%; Pred. No. 5, 2e-174;
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DB 78 vvitsgkgvgktttntanvglsaryfsvaldadlglnldllglenvntcyevi 137
QY 121 NGDCRLDQALVRDKRMSNFELLCISKRPSKLPMGFGSKALEMVLDAKTRPESDPDTII 180
DB 138 ngdcridqalvrdrkwnsfellciskprsklpmgfgskalewlvdaiktrpesspdtfii 197
QY 181 DCPAGIDAGRTTAPNEAVLWTPDTALRQADRVTGLECGGIRPKIVRVRPDM 240
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QY 241 IKGEDMMSVLDVOEMLSILGVPEDSEVIRSTRNGFPVLNRPPTLAGLAFQAAARL 300
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RESULT 3
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ID AA012922 standard; Protein; 326 AA.
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AC AA012922;
XX
DT 17-OCT-2000 (first entry)
XX

Arabidopsis thaliana protein fragment SEQ ID NO: 12222.

Protein Identification: signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

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Query Match 99.6%; Score 1648; DB 21; Length 326;

Best Local Similarity 99.7%; Pred. No. 2,2e-173; Mismatches 1; Indels 0; Gaps 0;

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DB 1 masrlstnhsqslpslsoktillssprlvnnrsrsvqvfnpkrlagelptl 60
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DB 61 vitsgkgvktttavngslarvgsvvaiddadlgirndlliglenrvnvcvevt 120
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DB 61 vltsggvgvgtttanvgislavgsvaiddadlgirndlliglenrvnvcvevt 120
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AC AAG12921;
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 12221.
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
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XX 05-MAR-1999; 99US-0123180.
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Query Match 99.6%; Score 1648; DB 21; Length 344;
Best Local Similarity 99.7%; Pred. No. 2,4e-173;
Matches 325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX AAG12923;
AC AAG12923;
XX 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SPQ ID NO: 12223.
XX KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
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PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
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PR 18-JUN-1999; 99US-0139456.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
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PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
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PR 24-JUN-1999; 99US-0140695.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 12-JUL-1999; 99US-0142977.
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PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 22-JUL-1999; 99US-0145085.
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PR 23-JUL-1999; 99US-0145145.
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PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145313.
PR 27-JUL-1999; 99US-0145319.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.

[illegible]

PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
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 PR 10-JUN-1999; 99US-0138540.
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 PR 31-AUG-1999; 99US-0151438.
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 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
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 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155559.
 PR 28-SEP-1999; 99US-0156458.
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 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.

PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 53.7%; Score 888; DB 21; Length 174;
Best Local Similarity 100.0%; Pred. No. 8e-90;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 MGEGKALEWLVDAIKTRPESPDFTIIDCPAGIDAGFTAITPANEAVLVTPDITAI 212
Db 1 mgfsgkalewlvdaiktrpesspdftiidcpagidagftaitpaneavlvtpditai 60
QY 213 DADVTGLLEDDGTRIDIMYVRRTDMIKGEDMSVLDVOMLGLSLGVIPEDSEVIR 272
Db 61 dadvtglleddgtridimlvrtomikgedmmsvldvgemlgslilgvipedssevir 120
QY 273 STNGEFLVLNKPPTLAGLAEQAAMRLVEDDSMKAVVVEEPPKRGFFSFGG 326
Db 121 stngfvlvlknkptlaglafegaawrlvegdsnmkavveepkkrgrffsfgg 174

RESULT 7

AAV10990 standard; Protein: 294 AA.

AAV10990;

08-JUN-1999 (first entry)

H. pylori ORF 06ep11202_4569693_c2_28 cellular protein.

vacuole; probe; diagnostic; ORF; cell envelope protein;
secreted protein; cellular protein.

Helicobacter pylori.

MO9818323-A1.

07-MAY-1998.

28-OCT-1997; 97WO-US19575.

14-JUL-1997; 97US-0891928.

28-OCT-1996; 96US-0739150.

06-DEC-1996; 96US-0759739.

(ASTRA) ASTRA AB.

Alm RA, Smith D;

WPI: 1998-271811/24.

N-PSDB: AAX30457.

Helicobacter pylori nucleic acids and proteins - used to develop
products for the detection, prevention and treatment of H. pylori
infections

Claims 27, 31; Page 195; 279pp; English.

Recombinant or substantially pure preparations of H. pylori polypeptides
are disclosed, together with the nucleic acids encoding them. In all,
73 ORFs are shown. The proteins are variously cell envelope proteins,
secreted proteins or other cellular proteins. Vaccines containing at least
8 nucleic acids or proteins are claimed, as are probes containing at least
8 nucleotides from the nucleic acid sequences. The vaccines are useful
for treating or reducing the risk of H. pylori infections, and the
probes can be used diagnostically for detecting the presence of
Helicobacter in a sample. The products are also of use in screening
for compounds having the ability to interfere with the H. pylori life
cycle or to inhibit H. pylori infection.

Sequence 294 AA;

Query Match 13.5%; Score 224; DB 19; Length 294;
Best Local Similarity 29.1%; Pred. No. 4.4e-16;
Matches 87; Conservative 40; Mismatches 106; Indels 66; Gaps 11;

QY 55 GEPRIIVITSGKGVGTGTTTANVGLSLARYGSFVAVIDDLGRNLDLGLLENRVY 114
Db 25 gnt-kfaietsgkgygksnlsanlalslykkykvvgfddadiglanldvlgvntkn- 82
QY 115 TCVEVINGDCRLDQALVRKWSNELCISKPSKRLPMG-----FGKALEWLV 164
Db 83 -llhalkeaklg-----elicelepgjcllpgdsgeelkylsgaaeldrfv 129
QY 165 DAKTRPEG---SPDFTIIDCPAGIDAGFTAITPANEAVLVTPDITAIAPADAVTGL 221
Db 130 d-----eevylssldyivldgagltgafinasdevvltvcpasaitda-----y 178
QY 222 ECDGIR-----DINKIVNR-----RTDMIKGEDMSVLDVOMLGLSLGVIP 265
Db 179 aciknsknkdelfliamvqpkgralyerllfkvaknnlas-----lelhylgate 231
QY 266 EDSEVIRSTNGFPLVLNKPPTLAGLAEQAAMRLVEDDSMKAVVVEEPPKRGFFSFP 324
Db 232 nssllkryvrerklirkiapndlfsqslasllvskletgltl-----elipkeglskf 286

RESULT 8

AAW20738 standard; Protein: 297 AA.

AAW20738;

16-JUL-1997 (first entry)

H. pylori cytoplasmic protein, 06cp20302orf8.

Cytoplasmic; vaccine; prevention; treatment; infection; identification;
binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
duodenal ulcer disease; chronic gastritis; diagnosis; envelope.

Helicobacter pylori.

MO9640893-A1.

19-DEC-1996.

06-JUN-1996; 96WO-US09122.

01-APR-1996; 96US-0630405.

07-JUN-1995; 95US-0487032.

(ASTRA) ASTRA AB.

Berglindh OT, Smith D, Mellgaerd BJ;

WPI: 1997-052306/05.

N-PSDB: AAT67991.

Helicobacter pylori nucleic acid sequences and related
polypeptide(s) - useful for vaccines to treat or prevent H. pylori
infection, and to detect Helicobacter

Claim 61; Page 1154; 1481pp; English.

The present sequence is a Helicobacter pylori cytoplasmic protein.
The protein may be used in a vaccine to prevent or treat H. pylori
infection or to identify H. pylori polypeptide binding compounds,
useful as potential H. pylori life cycle activators or inhibitors.
The genomic sequence of H. pylori (ATCC 55679) was determined from
overlapping contigs generated by mechanically shearing the bacterial
DNA. The sequences were analysed for ORF of at least 180 nucleotides,
and the predicted coding regions defined by computer evaluation. To
identify likely H. pylori antigens for vaccine development, the amino
acid sequences predicted from various ORF were analysed for significant

DR WPI; 2000-376567/32.
 DR N-PSDB; AAA61510.
 XX New protein from *Agrobacterium vitis*, useful e.g. for imparting
 PT resistance to disease or stress to plants, is involved in production of
 PT a hypersensitive response -
 PS Claim 3; Page 112-113; 157pp; English.
 XX Sequences AAB1630-B1688 represent proteins from *Agrobacterium vitis*
 CC which elicit a hypersensitivity response (HR) in a plant. The invention
 CC also relates to nucleotide sequences (AAA61501-A61524) encoding the A.
 CC vitis HR elicitor proteins. The HR is a rapid, localised necrosis that
 CC is associated with the active defence of plants against many pathogens,
 CC and occurs when a pathogenic organism interacts with a nonhost plant
 CC (i.e. one in which intracellular bacterial growth and disease development
 CC do not occur). Like other HR elicitors, the A. vitis elicitor functions
 CC in non-host plants by causing a rapid hypersensitive response that
 CC results in walling-off and killing of the pathogen. On grape plants, the
 CC A. vitis elicitor induces a restricted necrosis of tissues, resulting in
 CC the death of plant cells and induction of pathogen resistance. A. vitis
 CC HR elicitor proteins, in non-infectious form, are used to treat plants or
 CC their seeds to impart resistance to disease, such as those caused by
 CC fungi, bacteria or viruses, and to enhance growth, e.g., to increase
 CC yield or to provide earlier germination or maturation. The proteins can
 CC also be used to control insects, to impart resistance to environmental
 CC stresses, e.g., cold, and to improve nutritional value, e.g., altered oil
 CC content. The same effects can be produced by producing transgenic plants
 CC or seeds by incorporation of DNA that encodes A. vitis HR elicitor
 CC proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding
 CC them, may allow control of previously untreatable diseases; provide
 CC systemic treatment; and eliminate the need for biological control agents
 CC or polluting chemicals.
 CC
 XX Sequence 388 AA:
 SQ
 Query Match 12.5%; Score 206; DB 21; Length 388;
 Best Local Similarity 25.9%; Pred. No. 6.7e-14;
 Matches 72; Conservative 48; Mismatches 100; Indels 58; Gaps 10;
 QY 60 IVVITSGGKGVKTTTANVGLSLARYGFSVAIDADGLRLNLDLLEENRVNYTCVEV 119
 DB 131 IIAVAGSGKGVKSTAVLALALANGILKVGILADAVGSPMPRIIGLSRPG----- 184
 QY 120 INGDRLDQALVRDRKWSNFELLCISKPSKLPMPGF---GKALEW-----LVDAK 168
 DB 185 -----qldgrll-vpmenygikams-----igflvdegatamiwrgpmvsalmgmrlr 230
 QY 169 TRPESPEFIITDCPAGIDAGFITAI--TPANFAVLVTPDITALRDADRVTGLLECDGI 226
 DB 231 evaweladlvavdmpgvgdaqltmaqgyvlavsvlscpdalalldatrgimfkvev 290
 QY 227 RDIKMIYNR-----VRTMI-----KGEDMMSVLDOENMLGSLGLVIEDSEVIR 272
 DB 291 pvlgyflemysfiapdtgrtydflfnggakae-----aaaiagpfliepltsire 342
 QY 273 STNRGFPVLNKPPTLAGLAFAEQAA---WRLVEODSMK 307
 DB 343 hsdagltprvseespaqlvyreialtrwreverhstr 380
 RESULT 11
 ID AAM20443
 ID AAM20443 standard; protein; 412 AA.
 XX AAM20443;
 AC AAM20443;
 DT 14-JUL-1997 (first entry)
 XX H. pylori cytoplasmic protein, 35163962.aa.
 DE Cytoplasmic; vaccine; prevention; treatment; infection; identification;
 KW

KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
 KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
 XX Helicobacter pylori.
 XX WO9640893-A1.
 XX 19-DEC-1996.
 XX 06-JUN-1996; 96WO-US09122.
 XX 01-APR-1996; 96US-0630405.
 XX 07-JUN-1995; 95US-0487032.
 XX (ASTR) ASTRA AB.
 XX Berglindh OT, Smith D, Møllgaard BL;
 DR WPI; 1997-052306/05.
 DR N-PSDB; AAT67616.
 PT Helicobacter pylori nucleic acid sequences and related
 PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
 PT infection, and to detect Helicobacter
 PS Claim 61; Page 617-618; 1481pp; English.
 XX The present sequence is a Helicobacter pylori cytoplasmic protein.
 CC The protein may be used in a vaccine to prevent or treat H. pylori
 CC infection or to identify H. pylori polypeptide binding compounds, useful
 CC as potential H. pylori life cycle activators or inhibitors. The genomic
 CC sequence of H. pylori (ATCC 55679) was determined from overlapping
 CC contigs generated by mechanically shearing the bacterial DNA. The
 CC sequences were analysed for ORF of at least 180 nucleotides, and the
 CC predicted coding regions defined by computer evaluation. To identify
 CC likely H. pylori antigens for vaccine development, the amino acid
 CC sequences predicted from various ORF were analysed for significant
 CC homology to other known or exported membrane proteins. Having identified
 CC and determined the sequences of interest, particular regions can be
 CC isolated from H. pylori by PCR amplification for recombinant polypeptide
 CC production, e.g. in E. coli hosts.
 CC
 XX Sequence 412 AA:
 SQ
 Query Match 12.0%; Score 198; DB 18; Length 412;
 Best Local Similarity 23.9%; Pred. No. 5.7e-13;
 Matches 79; Conservative 56; Mismatches 114; Indels 82; Gaps 12;
 QY 8 STNRGSLPSSLSQKTLISSPRFVNNPSRPSRVLDGFRKPE-----LAGETPR 59
 DB 92 sseetsaillrenliskamegkykalnldtkpp-----kpgqpkptcknlaknlkh 142
 QY 60 IVVITSGGKGVKTTTANVGLSLARYGFSVAIDADGLRLNLDLLEENRVNYTCVEV 119
 DB 143 vvmlassgkygystvslstslanlqkvglldadvgnlprimglq----- 192
 QY 120 INGDRLDQALVRDRKWSNFELLCISKPSKLPMPGF---GKALEWLVDAKTRPE- 172
 DB 193 -nadvimpsgkklipkafg-----vsmsmgillydegglivrgpmlmaladq 241
 QY 173 -----GSPDFIITDCPAGID--AGFTAITPANFAVLVTPDITALRDADR----- 216
 DB 242 mlsdliwgldlvavdmprrncrcahaavplsgltvcpqylvsldakrslmfk 301
 QY 217 -----VTGGLLE-----CDGIRDIKMIYNRVDMIKGEDMMSVLDOENMLGSLGLVIE 266
 DB 302 lhiplagivemngstveclck-----keselfgsmmgsl--leayngllaklpl 350
 QY 267 DSEVIRSTNRGFPVLNKPPTLAGLAFAEQAA 297
 DB 351 epkvrllgdkgeplivshpitsvsaklfekma 381

PR	04-AUG-1999;	99US-0147302;
PR	05-AUG-1999;	99US-0147192;
PR	05-AUG-1999;	99US-0147260;
PR	06-AUG-1999;	99US-0147303;
PR	06-AUG-1999;	99US-0147416;
PR	09-AUG-1999;	99US-0147493;
PR	09-AUG-1999;	99US-0147935;
PR	10-AUG-1999;	99US-0148171;
PR	11-AUG-1999;	99US-0148319;
PR	12-AUG-1999;	99US-0148341;
PR	13-AUG-1999;	99US-0148565;
PR	13-AUG-1999;	99US-0148684;
PR	16-AUG-1999;	99US-0149368;
PR	17-AUG-1999;	99US-0149175;
PR	18-AUG-1999;	99US-0149426;
PR	20-AUG-1999;	99US-0149722;
PR	20-AUG-1999;	99US-0149723;
PR	20-AUG-1999;	99US-0149929;
PR	23-AUG-1999;	99US-0149902;
PR	23-AUG-1999;	99US-0149930;
PR	25-AUG-1999;	99US-0150566;
PR	26-AUG-1999;	99US-0150884;
PR	27-AUG-1999;	99US-0151065;
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Run on: February 11, 2002, 13:31:13 ; Search time 12.59 Seconds

(Without alignments)
582.690 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	88.5	5.4	264	3	US-08-468-544-16
4	88.5	5.4	519	3	US-08-997-445D-2
5	88	5.3	376	4	US-09-461-474-6
6	88	5.3	732	5	PCR-US95-17026-2
7	87	5.3	249	1	US-08-597-236-5
8	87	5.3	249	1	US-08-746-682A-5
9	86.5	5.2	416	3	US-09-320-878-18
10	86.5	5.2	416	4	US-09-105-537-39
11	85.5	5.2	1068	4	US-09-085-199B-11
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16	82.5	5.0	396	4	US-09-461-474-2
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25	79	4.8	1041	3	US-08-473-446-4
26	78.5	4.7	371	2	US-08-837-593-8
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30	78	4.7	937	1	US-08-253-155A-31	Sequence 31, Appl
31	78	4.7	3567	2	US-07-642-734C-4	Sequence 4, Appl1
32	78	4.7	3567	3	US-08-439-009A-4	Sequence 4, Appl1
33	77.5	4.7	325	4	US-09-088-435-1	Sequence 1, Appl1
34	77.5	4.7	2037	4	US-09-306-998-3	Sequence 3, Appl1
35	77	4.7	420	4	US-09-066-047-8	Sequence 8, Appl1
36	77	4.7	553	4	US-09-413-814-3	Sequence 3, Appl1
37	76	4.6	694	1	US-08-164-839-4	Sequence 4, Appl1
38	76	4.6	694	1	US-08-583-799-4	Sequence 4, Appl1
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42	75.5	4.6	2616	6	US-08-948-176-26	Sequence 26, Appl1
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44	75	4.5	678	1	US-08-435-434-2	Sequence 2, Appl1
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ALIGNMENTS

RESULT 1
US-08-969-644-16
Sequence 16, Application US/08969644
Patent No. 6096519
GENERAL INFORMATION:
APPLICANT: Ratti, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario F.
APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM: RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,644
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,152
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A00314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1677-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-969-644-16

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Best Local Similarity	24.0%	Preg	No.	0.09			
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; Sequence 16, Application US/08444189

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; GENERAL INFORMATION:
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; APPLICANT: Ratti, Giulio
;
; APPLICANT: Comanducci, Maurizio
;
; APPLICANT: Tocco, Mario D

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APPLICANT: Giuliani, Marzia M.
TITLE OF INVENTION: PCID PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
TITLE OF INVENTION: THEM; RECOMBINANT PLASTIDS FOR THE EXPRESSION OF SAID

TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

CITY: Falls Church
STATE: Virginia
COUNTRY: USA

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; MEDIUM TYPE: FLOPPY
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; OPERATING SYSTEM: DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,189
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,528
FILING DATE:

REPLICATION NUMBER: US/01/591,312
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:

FILING DATE: 07-FEB-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Svensson, Leonard R.

REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
FAX: 703-241-2040

INFORMATION FOR SEQ ID NO: 16:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-444-189-16

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Best Local	24.0%	Pred.	No.	0.05			
Matches	44	Conservative	26	Mismatches	78	Indels	35
						Gaps	7

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? GENERAL INFORMATION:
? APPLICANT: Ratti, Giulio
? APPLICANT: Comanducci, Maurizio
? ATTORNEY:

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1 APPLICANT: Giuliano, Marzia M.
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4 TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
5 TITLE OF INVENTION: THEM. PROMINANT PLASTIDS FOR THE EXPRESSION OF SAID

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STATE: Virginia
CITY: Falls Church
COUNTRY: USA

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;

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; SOFTWARE: Patentin Release #1.0, Version #1.23
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/468,544
;
; FILING DATE: 06-JUN-1995

```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,820
FILING DATE: 28-FEB-1991

APPLICATION NUMBER: 11 MI 91A000314
 FILING DATE: 07-FEB-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Svensson, Leonard R.

REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300

TELE: 248343
; INFORMATION FOR SEQ ID NO: 16

Query Match	5.4%	Score 88.5	DB 3	Length 519
Best Local Similarity	19.3%	Pred. No. 0.27		
Matches 53; Conservative	36	Mismatches 76	Indels 107	Gaps 12

1 RESULT 6
 2 PCT-US95-17026-2
 3 Sequence 2, Application PC/TUS9517026
 4 GENERAL INFORMATION:
 5 APPLICANT: Zymogenetics, Inc.
 6 APPLICANT: 1201 Eastlake Avenue East
 7 APPLICANT: Seattle
 8 APPLICANT: WA
 9 APPLICANT: USA
 10 TITLE OF INVENTION: 98102
 11 NUMBER OF SEQUENCES: 13
 12 CORRESPONDENCE ADDRESS:
 13 ADDRESS1: Zymogenetics, Inc.
 14 STREET: 1201 Eastlake Avenue East
 15 CITY: Seattle

STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17026
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-18PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 732 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-17026-2

Query Match 5.3%; Score 88; DB 5; Length 732;
Best Local Similarity: 24.2%; Pred. No. 0.53;

Matches 72; Conservative 38; Mismatches 94; Indels 94; Gaps 20;

QY 34 NPSRRSPRSLVLOFNKPE---LAGETPRIVITSGKGVGKTTTANGLST----- 83
DB 255 NPIKSVRSVGSAM-IRAKDDEGVYAGSMQNVAY-----GVPSAMTGSVDILLETSSQK 308
QY 84 -ARGFSVALDADLGLNLDL-LGLENRV--NTCCEVINGDCRLD-----OA 129
DB 309 PVRGQGCWVF---AGVNTFLRCGIPARVVTNYSADNDANQLDLEEDGNVNSK 364
QY 130 LVPRDRMSNFEELCTSK---PRSKLPMGFGKALEMVDALKTREPSDPDIIIDPACI 186
DB 365 LTKDSVM-NYH--CMNEAMMRPDLPGVFGG---WQY--VISTFOENDGMYRCGFASV 415
QY 187 -----DAGFTAITPANEAVLVTPDITALRDADRVTLLEC----- 223
DB 416 QAIKHGVCFQFADAFVFA--EVNSDLVY---VPAKKDGHVVALDTTHIGKLIYTK 469
QY 224 ---DGIDIKIIVNRVRDMK---GPDMSVLDOEMLG---LSLGVIPEDSEV 270
DB 470 IGGDKMDI-----TDYKFOEGOEERLLETAMYGAKKALNTEGVLSKSDV 519

RESULT 7

US-08-597-236-5
Sequence 5, Application US/08597236
Patent No. 573765
GENERAL INFORMATION:
APPLICANT: STINGELE, Francesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,236
FILING DATE:
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-597-236-5

Query Match 5.3%; Score 87; DB 1; Length 249;
Best Local Similarity: 20.8%; Pred. No. 0.12;
Matches 48; Conservative 40; Mismatches 79; Indels 64; Gaps 10;

QY 41 IRSVLOFNKPE-----LAGETPRIVITSGKGVGKTTTANGLSLARYGES 89
DB 7 VKSKVDPRAKTEEYNAIRTIQSFSGAMQKVIATISVAGSKSISVNLAIISFASVIR 66
QY 90 VVALDADLGLNLDDLGLENRVYTCVEVINGDCRLDQALVRDKRWSNF-----EL 141
DB 67 TLILDAE--TRN-----SVLSGTFKSNPEY---KGLSNFLSGNADLNET 105
QY 142 LC---IS-----KPSKLPMGFGKALEMVDALKTREPSDPDIIIDC-PAG 185
DB 106 ICOTDISGLDVYASGPVPNPPTSLQ---NDNFRHMEVARS---CYDVIIIDTPVPG 157
QY 186 IDAGFTAITPANEAVLVTPDITALRDADRVTLLECDDGIRDKIMVNRV 236
DB 158 LVIDAVIARIQADASLVLTEAGIKRRFYTKAVQLVESGSQFLGVYLVNKV 208

RESULT 8

US-08-746-682A-5
Sequence 5, Application US/08746682A
Patent No. 5766184
GENERAL INFORMATION:
APPLICANT: STINGELE, Francesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,682A
FILING DATE: 14-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,236
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: FARUCCI A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-746-682A-5

Query Match 5.3%; Score 87; DB 1; Length 249;
Best Local Similarity 20.8%; Pred. No. 0.12;
Matches 48; Conservative 40; Mismatches 79; Indels 64; Gaps 10;

QY 41 IRSVLOGRKPE-----LAGETPRIVVITSGKGVKTTTANVGLSLARYGFS 89
DB 7 VKSKVDAKKEEYMAIRTIQESGAQKVAISSVEGEGKSMISVLAISFASVGLR 66
QY 90 VVAIDADGLRDLGLLENRVNTQVEVINGDCRLDQALVRDRKSNF-----EL 141
DB 67 TLIDAE--TFN-----SVLSGTFKSNPY--KGLSNFLSGMDLNET 105
QY 142 LC-----IS-----KPRSKLPMGFGKALEMVDALKTREGSPDFIITDC-PAG 185
DB 106 ICQTDISGLDVIASGVPNPFTSLQ---NDNFRHLMVARS---CYDYIITDPPVG 157
QY 186 IDAGFTAITPANAEVAVTTPDITLRDADRVYTGLECGIDIKIMVNRV 236
DB 158 LVDAVIAHQADASLVTEAGKIRRYTKAVEQLVESGSGFLGVLVKLV 208

RESULT 9
US-09-320-878-18
Sequence 18, Application US/09320878A
Patent No. 6117659

GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
TITLE OF INVENTION: RECOMBINANT NARHONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
CURRENT FILING DATE: 1999-05-27
EARLIER FILING DATE: 1999-05-27
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 416
TYPE: PRT
ORGANISM: Streptomyces venezuelae
US-09-320-878-18

Query Match 5.2%; Score 86.5; DB 3; Length 416;
Best Local Similarity 22.2%; Pred. No. 0.31;
Matches 42; Conservative 31; Mismatches 73; Indels 43; Gaps 7;
QY 125 RLDQALVRDRKSNFELLCISKRSLPMGFGKALEMVDALKTREGSPDFIITDCPA 184

DB 102 RLKLVAREFTMRVELL---RPVQ-----EIVDGLVDAMLAADGRADLM----- 145
QY 185 GIDAGFTAITPANAEVAVTTPDITLR-----DADRTGLLECCGIDIKIMV 233
DB 146 -ESLAMPITVVISSELLGVPEPRAAFRVWTDVAFVPPDDPAQOTAMKMSGY--LSRLI 202
QY 234 NRVRTDMIKGEDMMSV-----LDVOEMLGLSLGLVPEDESEVIRSTNGRFPVLV 282
DB 203 DSKRGQ--DGEDLSALVRTSDEDSRLTSEELGMHILLVAGHETVNLANGVYALL 260
QY 283 NKPPITAGL 291
DB 261 SHPDQLAAL 269

RESULT 10
US-09-105-537-39
Sequence 39, Application US/09105537A
Patent No. 6265202

GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600,438051
CURRENT FILING DATE: 1998-06-26
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 416
TYPE: PRT
ORGANISM: Streptomyces venezuelae
US-09-105-537-39

Query Match 5.2%; Score 86.5; DB 4; Length 416;
Best Local Similarity 22.2%; Pred. No. 0.31;
Matches 42; Conservative 31; Mismatches 73; Indels 43; Gaps 7;

QY 125 RLDQALVRDRKSNFELLCISKRSLPMGFGKALEMVDALKTREGSPDFIITDCPA 184
DB 102 RLKLVAREFTMRVELL---RPVQ-----EIVDGLVDAMLAADGRADLM----- 145
QY 185 GIDAGFTAITPANAEVAVTTPDITLR-----DADRTGLLECCGIDIKIMV 233
DB 146 -ESLAMPITVVISSELLGVPEPRAAFRVWTDVAFVPPDDPAQOTAMKMSGY--LSRLI 202
QY 234 NRVRTDMIKGEDMMSV-----LDVOEMLGLSLGLVPEDESEVIRSTNGRFPVLV 282
DB 203 DSKRGQ--DGEDLSALVRTSDEDSRLTSEELGMHILLVAGHETVNLANGVYALL 260
QY 283 NKPPITAGL 291
DB 261 SHPDQLAAL 269

RESULT 11
US-09-085-199B-11
Sequence 11, Application US/09085199B
Patent No. 6235879
GENERAL INFORMATION:
APPLICANT: Hayden, Michael R.
APPLICANT: Hackam, Abigail
APPLICANT: Hug, A.H.M. Mahubul
APPLICANT: Chopra, Vikramjit Singh
APPLICANT: Kalchman, Michael
TITLE OF INVENTION: Apoptosis Modulators That Interact with the
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:

```

ADDRESS: Oppedahl & Larson
STREET: PO Box 5270
CITY: Frisco
STATE: CO
COUNTRY: USA
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
OPERATING SYSTEM: MS DOS 5.0
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UBC-P-013052
TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2052
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: no
ORIGINAL SOURCE:
ORGANISM: mouse
FEATURE:
OTHER INFORMATION: Huntington-interacting protein -mhipla
US-09-085-199B-11

Query Match
Best Local Similarity 5.2%; Score 85.5; DB 4; Length 1068;
Matches 69; Conservative 52; Mismatches 147; Indels 65; Gaps 14;

QY 12 QSLPLPSLSOKTLISPFVNP5-RSPISRVLOFN-----RKPELAGETPR1 60
DB 731 RALEVVGLOQOQYVLRNQ-----PSLMRAPLOGIILQLODLPKSIDVQBELGAMVDKE 786
QY 61 VVITSGGKGVKTTTANVGLSLARYGSVAIDDLGIRN-----LDLLGLENVY 112
DB 787 MAATS--AAIEDAVRIEDMMSOARHSSGVKLEVENRILNCTDLMKAIIRLIVMTSTSL 844
QY 113 NYTCVEYINGCDRLDOALVRKMSNFELLCISKRSLPMPGFGKALEMLVDAKTRPE 172
DB 845 QKEIVESGRGATQOEFLAKNSWTE-GLISASK-----AVGWSATQLVESADKVVLMHG 898
QY 173 GSPDEIITIDCPAGIDAGFTTAITPANEAVALVTPDITALLRADRYTGLLECDGIDIKMI 232
DB 899 KYEELIV--CSHEI-----AASQVLAASKVKANKNSPHLSRIQES--RTVNR 945
QY 233 VNRRTMIGEDMSVIDVQEMGLSLGVTPEDSEV-INSTNGCFPLVNLKPPTLAQL 291
DB 946 AANVASTKSGQEQIEDRDYDFSLIKLKQEMETQVR-----VLELEKTL--- 994
QY 292 AFEOAMRLVEODSMKAVM-----EEEPK 317
DB 995 --EAERYRLGELRKOHVVLAVGKGTPEEPESR 1025

RESULT 12
5223423-2
; APPLICANT: FRANCHINI, GENOVERFA, WONG-STAAI, FLOOSIE,
; GALLO, ROBERT
; TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
; HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
; NUMBER OF SEQUENCES: 4

```

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/331,212
FILING DATE: 03-31-1989
; SEQ ID NO: 2
; LENGTH: 3077
5223423-2

Query Match
Best Local Similarity 5.0%; Score 83.5; DB 6; Length 3077;
Matches 61; Conservative 48; Mismatches 122; Indels 53; Gaps 15;

QY 57 TPRLVITSGKGVKTTTANVGLSLARYGSVAIDDLGLRNDLLGLENRYTC 116
DB 2037 TPLCVTMNCANSTESAVATTSQGPMDNDPCIQLNKCSGLREEDM--VECFNMKG 2093
QY 117 VEINGDCRLDOALVRKMSNFELLC--ISKPSKLPMPGFGKAL-----EWLVD 165
DB 2094 LE-----LDKKQYSETWSKDYCESDSTDRKRCYMNCNVSITESCDKHYW--D 2144
QY 166 ALKTRPESGSPFTIIDCPAGIDAGFTTAITPANEAVALVTPDITALLRADRYTGLLECDG 225
DB 2145 AMRRYCAPPGFVLLRCNDYVSGF---EPNCSKVAVST--CTRMETQPTWL-----G 2194
QY 226 IROIKMIVNRVTD-----MIKGEDMSVLDVQEMGLSLGVTPEDSEVTRST--NRG 277
DB 2195 F-----NGRAENRRTYIHGGRDNRTIISLNKYNLTLICRRPENTVPTILMSGR 2247
QY 278 F--PLVINKPPTLAGLAPEQAMRLVEODSMKAVWEEEPKRG 319
DB 2248 FHSQKIINKKRRQAMCRF-KGEMREAME-VKQTLV-KHPRYKG 2288

RESULT 13
US-08-416-603-4
; Sequence 4, Application US/08416603
; Patent No. 5866780
; GENERAL INFORMATION:
; APPLICANT: Law, Marcus
; APPLICANT: Hebara, Iedare
; TITLE OF INVENTION: Readdick, Bradford B.
; TITLE OF INVENTION: Maize Chlorotic Dwarf Virus Genome and
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanichik & Saliwanichik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,603
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeffrey
REGISTRATION NUMBER: 35,589
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3457 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-416-603-4

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Query Match 5.0%; Score 83.5; DB 2; Length 3457;

Best Local Similarity 25.1%; Pred. No. 21; Matches 53; Conservative 30; Mismatches 87; Indels 41; Gaps 14;

18 SLSOKTLISSPRVNNRSRSPISVL-QFNKPE-LAGETPRIVITSGKGVGKTTT 75

2888 TSAATKTSI-----RKSRIHGLVGEIRTEPSILHAHPRL-----PKDKISKMDP 2932

QY 76 TANGLSARGFVSVALDADGLNLD-----LLGLENRVYTCY---EV-INGDCRLD 127

2933 VIEASM--KYGSRITPEPVQDILEVDHLSKMLANCENSKKKRQVNNLEIGING---ID 2986

QY 128 QALVRDKMSNFELCLISK-PRSK-LPMFGSKALEMLVDALKTRPGSPDFIIDCPAG 185

2987 QS-----DVMQGLEMDTSSGMPYAKRRKPYGAAGK--KWLFEQGTYPYSGKPRVYFGD--AG 3038

QY 186 IDAGFITAITPANEAVALVTPDITLADADR 216

DB 3039 LIESYNSMGEAKGKISPTVYIECAKDERR 3069

RESULT 14

US-08-896-320-1

Sequence 1, Application US/08896320

Patent No. 5871971

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Corley, Neil C.

APPLICANT: Shah, Purni

TITLE OF INVENTION: HUMAN DEVELOPMENTALLY REGULATED

TITLE OF INVENTION: GTP-BINDING PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/896.320

FILING DATE: Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0344 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 367 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: CARDNOT01

CLONE: 281964

US-08-896-320-1

Query Match 5.0%; Score 82.5; DB 2; Length 367;

Best Local Similarity 25.4%; Pred. No. 0.73; Matches 43; Conservative 20; Mismatches 37; Indels 69; Gaps 11;

QY 45 LQNRKPELAGETPRIVITSGKGVGKTTTANVGLS-----LARYGFSVAIDADL 97

DB 170 IRLMSKP-----PNIEFKKKDKGGINLTATCPSEDAETVKSILAEKIH---NADV 219

QY 98 GLRN-----LDLLGLENRVNTCVENVNGDCRLDQALVAD-----K 134

DB 220 TLRSDATADDLIDVVEG--NRYIYPCIVLVN---KIDISIEEDLIYKVPCHVISAHH 274

QY 135 RWSNFELCLISKPRSKLPMFGSKALEMLVDALK-----TRPGS-PDF 177

DB 275 RW-NFDDL-----LEKIMDWLKLVRITRKRGQLPDY 305

RESULT 15

US-08-896-320-3

Sequence 3, Application US/08896320

Patent No. 5871971

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Corley, Neil C.

APPLICANT: Shah, Purni

TITLE OF INVENTION: HUMAN DEVELOPMENTALLY REGULATED

TITLE OF INVENTION: GTP-BINDING PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/896.320

FILING DATE: Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0344 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 367 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: Genbank

CLONE: 220507

US-08-896-320-3

Query Match 5.0%; Score 82.5; DB 2; Length 367;

Best Local Similarity 25.4%; Pred. No. 0.73; Matches 43; Conservative 20; Mismatches 37; Indels 69; Gaps 11;

QY 45 LQNRKPELAGETPRIVITSGKGVGKTTTANVGLS-----LARYGFSVAIDADL 97

```

Db 170 IRLNSKP-----PNIGFKKKDKGINTLTFATCPQSELDATVKSILAEYKH-----:|:
OY 98 GLRN-----IDLILGLENRVNYTCVEVINGDCRILDQALVRD-----K 134
Db 220 TLRSDATADDLIDVVEG--NRVYIPCIYVLN--KIDQISIEELDIYKVPHCVPISAH 274
OY 135 RWSNEELICISKPRSKLPMGFGKALEMLVDALK-----TRPEGS-PDF 177
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Search completed: February 11, 2002, 13:31:36
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